

RESULT 5

AAV08697

ID AAV08697 standard; protein; 469 AA.

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AC

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15-JUN-2007 (revised)

DT 31-MAR-1999 (first entry)

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DE

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KW GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis;

KW peptic ulcer disease; BOND_PC; ATP synthase F1, subunit beta (atpD);

KW ATP synthase F1, subunit beta (atpD) [Helicobacter pylori 26695];

KW ATP synthase subunit B;

KW ATP synthase subunit B [Helicobacter pylori 26695]; G0166; G05524;

KW G06754; G06810; G06811; G08553; G015078; G015986; G015992; G016020;

KW G016021; G016469; G016787; G017111; G042777; G045261; G046872; G046933;

KW G046961.

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OS

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PN V0843478- A1.

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PD

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08- OCT- 1998.

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PF

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01- APR- 1998; 98WD- US006371.

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PR

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PR

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PA

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PI

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DR

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PT

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PS

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SQ

Helicobacter pylori.

01- APR- 1998; 98WD- US006371.

01- APR- 1997; 97US- 00833457.

24- JUN- 1997; 97US- 00881227.

29- JUL- 1997; 97US- 00902615.

(INMR) MERIEUX CRAVAX PASTEUR MERIEUX SERUMS.

(HUMA-) HUMAN GENOME SCI INC.

Kleanthous H, Al-Garawi A, Miller C, Torib J, Comen RP;

VPI: 1998- 542293/ 46.

N- PSDB; AAX14416.

PC: NCBI; gi2493023.

PC: SW SSPLIT; P55988.

PC: BOND; 18005, 18396.

New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases.

Claim 8; Page 1456-1458; 2054pp; English.

This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for detection and diagnosis

Revised record issued on 15-JUN-2007 : Enhanced with precomputed information from BOND.

Sequence 469 AA;

10595909

Best Local Similarity 79.5%

Matches 369; Conservative 36; Mismatches 59; Indels 0; Gaps 0;

Qy 1 MQGF SQVLGPVVDVDFNDYLPQ NEAI VVNFSEGGKHKLVLEVAHLGDNRVRTI AMD 60
 Db 4 MEGKI QVLGPVVDVEFESYLPAL FEALDI NFEVNGVQKSLVLEVAHLGDNRVRAI AMD 63

Qy 61 MTDGLVRGLKAEALGAPI SVPVGEKVLGRI FNVTDGLI DEGEEL SFDKKWAI HRDPPAFE 120
 Db 64 MTEGLVRNQI KARGKI EVPVGEEVLGRI FNVGESI DNLLEPLKPSLTWPI HRKAPSFE 123

Qy 121 DGSTKSEI FETGI KVVDLLAPYAKGGKVLFGGAGVGKTVI MELI HINAFKHSGYSVFA 180
 Db 124 CGSTKTEMFETGI KVI DLLAPYSKGGKVLFGGAGVGKTVI MELI HINAYKHNGYSVFA 183

Qy 181 GVGERTREGNDLYNEMKESNVLDKVALCYGQMNPPGARNRI ALTGLTMAEYFRDEMGLD 240
 Db 184 GVGERTREGNDLYFEMKEGGVLDKVALCYGQMNPPGARNRI AFTGLTMAEYFRDEKGLD 243

Qy 241 VLMFI DNI FRFSQSGSEMSALLGRI PSAVGYOPTLASEMGKFCERI TSTKKGSI TSVQAV 300
 Db 244 VLMFI DNI FRYAQSGAEMSALLGRI PSAVGYOPTLAGEMGKLCERI ASTKKGSI TSVQAV 303

Qy 301 YVPADDLTDPAATVFAHLDTATVLRNRI AEKG YPAVDPLDSTSRLDPNI GEEHYKV 360
 Db 304 YVPADDLTDPAASVFAHLDTATVLRNRI AEKG YPAVDPLDSTSRI LSPQI GEKHYEV 363

Qy 361 ARGVGSVLQKYKDLQDI AI LGVDELSEEDKLVERARKI EKFLSQPFFVAEVFTGSPGK 420
 Db 364 ATGI QVQLQKYKDLQDI AI LGVDELSEEDKKTVERARKI EKFLSQPFFVAEVFTGSPGK 423

Qy 421 YI SLEDTI AGFKGI LEGKYDHLPENAFYMWGNI DEAI AKADKLK 464
 Db 424 YVTLGETLEGFGG LEGKYDHI PENAFYMWGSI QEVLEKAKNMK 467